

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Hawkins, Phillip R.
Hillman, Jennifer L.
Lal, Preeti
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN SERINE
CARBOXYPEPTIDASE
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0241 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: MPHGN0T03
 - (B) CLONE: 443004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15
 Pro Gly Pro Cys Asp Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
 20 25 30
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45
 Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60
 Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Asp Phe Leu Thr Val
 65 70 75 80
 Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
 85 90 95
 Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Glu Pro
 100 105 110
 Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
 115 120 125
 Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
 130 135 140
 Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
 145 150 155 160
 Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
 165 170 175
 Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
 180 185 190
 Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
 195 200 205
 Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
 210 215 220
 Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
 225 230 235 240
 Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
 245 250 255
 Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
 260 265 270
 Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
 275 280 285
 Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
 290 295 300
 Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
 305 310 315 320
 Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
 325 330 335
 Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
 340 345 350
 Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365
 Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380
 Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400
 Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415
 Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Gly Val Ala Gly Tyr
 420 425 430
 Ile Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly
 435 440 445
 His Thr Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn

450 455 460
 Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MPHGN0T03
 (B) CLONE: 443004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCGCTGCA	AGGACAACCG	GCTGGGGTCC	TTGCGCGCCG	GGCTCAGGGA	GGAGCACCGA	60
CTGCGCCGCA	CCCTGAGAGA	TGGTTGGTGC	CATGTGGAAG	GTGATTGTTT	CGCTGGTCCCT	120
GTTGATGCCT	GGCCCCCTGT	ATGGGCTGTT	TCACTCCCTA	TACAGAAGTG	TTTCCATGCC	180
ACCTAAGGGA	GACTCAGGAC	AGCCATTATT	TCTCACCCCT	TACATTGAAG	CTGGGAAGAT	240
CCAAAAAGGA	AGAGAATTGA	GTTTGGTCCG	TCCTTTCCCA	GGACTGAACA	TGAAGAGTTA	300
TGCCGACTTC	CTCACTGTGA	ATAAGACTTA	CAACAGCAAC	CTCTTCTTCT	GGTCTTCCC	360
AGCTCAGATA	CAGCCAGAAG	ATGCCCCAGT	AGTTCTCTGG	CTACAGGGTG	AGCCGGGAGG	420
TTCATCCATG	TTTGGACTCT	TTGTGGAACA	TGGGCCTTAT	GTTGTCACAA	GTAACATGAC	480
CTTGCGTGAC	AGAGACTTCC	CCTGGACCAC	AACGCTCTCC	ATGCTTTACA	TTGACAATCC	540
AGTGGGCACA	GGCTTCAGTT	TTACTGATGA	TACCCACGGA	TATGCAGTCA	ATGAGGACGA	600
TGTAGCACGG	GATTTATACA	GTGCACTAAT	TCAGTTTTTC	CAGATATTTT	CTGAATATAA	660
AAATAATGAC	TTTTATGTCA	CTGGGGAGTC	TTATGCAGGG	AAATATGTGC	CAGCCATTGC	720
ACACCTCATC	CATTCCCTCA	ACCCTGTGAG	AGAGGTGAAG	ATCAACCTGA	ACGGAATTGC	780
TATTGGAGAT	GGATATTCTG	ATCCCGAATC	AATTATAGGG	GGCTATGCAG	AATTCCTGTA	840
CCAAATTGGC	TTGTTGGATG	AGAAGCAAAA	AAAGTACTTC	CAGAAGCAGT	GCCATGAATG	900
CATAGAACAC	ATCAGGAAGC	AGAACTGGTT	TGAGGCCTTT	GAAATACTGG	ATAAACTACT	960
AGATGGCGAC	TTAACAAGTG	ATCCTTCTTA	CTTCCAGAAT	GTTACAGGAT	GTAGTAATTA	1020
CTATAACTTT	TTGCGGTGCA	CGGAACCTGA	GGATCAGCTT	TACTATGTGA	AATTTTTGTC	1080
ACTCCAGAG	GTGAGACAAG	CCATCCACGT	GGGGAATCAG	ACTTTTAATG	ATGGAATAT	1140
AGTTGAAAAG	TACTTGCGAG	AAGATACAGT	ACAGTCAGTT	AAGCCATGGT	TAAGTAAAT	1200
CATGAATAAT	TATAAGGTTT	TGATCTACAA	TGGCCAACGT	GACATCATCG	TGGCAGCTGC	1260
CCTGACAGAG	CGCTCCTTGA	TGGGCATGGA	CTGGAAAAGGA	TCCCAGGAAT	ACAAGAAGGC	1320
AGAAAAA	AAAGTTTGGA	AGATCTTTAA	ATCTGACAGT	GGAGTGGCTG	GTTACATCCG	1380
GCAAGTGGGT	GACTTCCATC	AGGTAATTAT	TCGAGGTGGA	GGACATACTT	TACCCATATGA	1440
CCAGCCTCTG	AGAGCTTTTG	ACATGATTAA	TCGATTCATT	TATGGAAAAG	GATGGGATCC	1500
TTATGTTGGA	TAAACTACCT	TCCCAAAAGA	GAACATCAGA	GGTTTTTCATT	GCTGAAAAGA	1560
AAATCGTAAA	AACAGAAAAT	GTCATAGGAA	TAAAAAATT	ATCTTTTCAT	ATCTGCAAGA	1620
TCTTTTTCAT	CAATAAAAAT	TATCCTTGAA	ACAAAAA	AAAGAAAAAG		1670

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT01
 (B) CLONE: 566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1				5					10					15	
Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	His	Ser	Leu	Tyr	Arg	Ser	Val	Ser
			20					25					30		
Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
			35				40					45			
Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
	50					55					60				
Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Xaa	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115				120						125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Xaa	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200						205		
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
		210				215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225				230						235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260				265						270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys
		355					360					365			
Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn
		370				375					380				
Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu
385				390						395					400
Met	Gly	Met	Asp	Trp	Lys	Gly	Ser	Gln	Glu	Tyr	Lys	Lys	Ala	Glu	Lys
				405					410					415	
Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala	Gly	Tyr	Ile
			420					425					430		
Arg	Gln	Val	Gly	Asp	Phe	His	Gln	Val	Ile	Ile	Arg	Gly	Gly	Gly	His
		435					440					445			
Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn	Arg

450 455 460
Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: MMLR3DT01
- (B) CLONE: 566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAAAGCTGGT	ACGCCTGCNG	GTNCCGGTCC	GGAATTCNCG	GGTNGACCCA	CGCGTCCGAN	60
CGACTGCGCC	GCACCCTGAG	AGATGGTTGG	TGCCATGTGG	AAGGTGATTG	TTTCGCTGGT	120
CCTGTTGATG	CCTGGCCCCCT	GTGATGGGCT	GTTTCACTCC	CTATACAGAA	GTGTTTCCAT	180
GCCACCTAAG	GGAGACTCAG	GACAGCCATT	ATTTCTCACC	CCTTACATTG	AAGCTGGGAA	240
GATCCAAAAA	GGAAGAGAAT	TGAGTTTGGT	CGGCCCTTTC	CCAGGACTGA	ACATGAAGAG	300
TTATGCCGGC	TTCTCACCG	TGAATAAGAC	TTACAACAGC	AACCTCTTCT	TCTGGTTCTT	360
CCCAGCTCAG	ATACAGCCAG	AAGATGCCCC	AGTAGTTCTC	TGGCTACAGG	GTGGGCCGGG	420
AGGTTTCATC	ATGTTWGGAC	TCTTTGTGGA	ACATGGGCCT	TATGTTGTCA	CAAGTAACAT	480
GACCTTGCCT	GACAGAGACT	TCCCCTGGAC	CACAACGSTC	TCCATGCTTT	ACATTGACAA	540
TCCAGTGGGC	ACAGGCTTCA	GTTTTACTGA	TGATACCCAC	GGATATGCAG	TCAATGAGGA	600
CGATGTAGCA	CGGGATTTAT	ACAGTGCAC	AATTCAGTTT	TTCCAGATAT	TTCTGAATA	660
TAAAAATAAT	GACTTTTATG	TCACTGGGGA	GTCTTATGCA	GGGAAATATG	TGCCAGCCAT	720
TGCACACCTC	ATCCATTCCC	TCAACCTGT	GAGAGAGGTG	AAGATCAACC	TGAACGGAAT	780
TGCTATTGGA	GATGGATATT	CTGATCCCGA	ATCAATTATA	GGGGGCTATG	CAGAATTCCT	840
GTACCAAAAT	GGCTTGTTGG	ATGAGAAGCA	AAAAAAGTAC	TTCCAGAAGC	AGTGCCATGA	900
ATGCATAGAA	CACATCAGGA	AGCAGAACTG	GTTTGAGGCC	TTTGAAATAC	TGGATAAACT	960
ACTAGATGGC	GACTTAACAA	GTGATCCTTC	TTACTTCCAG	AATGTTACAG	GATGTAGTAA	1020
TTACTATAAC	TTTTTGCGGT	GCACGGAACC	TGAGGATCAG	CTTTACTATG	TGAAATTTTT	1080
GTCACCTCCA	GAGGTGAGAC	AAGCCATCCA	CGTGGGGAAT	CAGACTTTTA	ATGATGGAAC	1140
TATAGTTGAA	AAGTACTTGC	GAGAAGATAC	AGTACAGTCA	GTTAAGCCAT	GGTTAACTGA	1200
AATCATGAAT	AATTATAAGG	TTCTGATCTA	CAATGGCCAA	CTGGACATCA	TCGTGGCAGC	1260
TGCCCTGACA	GAGCGCTCCT	TGATGGGCAT	GGACTGGAAA	GGTTCCCAGG	AATACAAGAA	1320
GGCAGAAAAA	AAAGTTTGGA	AGATCTTTAA	ATCTGACAGT	GAAGTGGCTG	GTTACATCCG	1380
GCAAGTGGGT	GACTTCCATC	AGGTAATTAT	TCGAGGTGGA	GGACATATTT	TACCCTATGA	1440
CCAGCCTCTG	AGAGCTTTTG	ACATGATTAA	TCGATTCAAT	TATGGAAAAG	GATGGGATCC	1500
TTATGTTGGA	TAAACTACCT	TCCCAAAAGA	GAACATCAGA	GGTTTTTCATN	T	1551

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCR01
- (B) CLONE: 770469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15
 Pro Gly Pro Cys Gly Gly Leu Phe His Ser Leu Tyr Arg Ser Val Ser
 20 25 30
 Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45
 Ile Glu Ala Gly Lys Ile Tyr Thr Gly Thr Asn Ser Val Phe Gln Ile
 50 55 60
 Phe Pro Glu Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr
 65 70 75 80
 Ala Gly Lys Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn
 85 90 95
 Pro Val Arg Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp
 100 105 110
 Gly Tyr Ser Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu
 115 120 125
 Tyr Gln Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys
 130 135 140
 Gln Cys His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu
 145 150 155 160
 Ala Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp
 165 170 175
 Pro Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe
 180 185 190
 Leu Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu
 195 200 205
 Ser Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe
 210 215 220
 Asn Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln
 225 230 235 240
 Ser Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu
 245 250 255
 Ile Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu
 260 265 270
 Arg Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys
 275 280 285
 Ala Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala
 290 295 300
 Gly Tyr Ile Arg Gln Val Gly Asp Phe His Gln Val Ile Ile Arg Gly
 305 310 315 320
 Gly Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met
 325 330 335
 Ile Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 340 345 350

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNCRT01
- (B) CLONE: 770469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGGCAAACC GGCTGGGGTC CTTGCGCGCC GCGGCTCAGG GAGGAGCACC GACTGCCCCG 60
 CACCCGTGAGA GATGGTTGGT GCCATGTGGA AGGTGATTGT TTCGCTGGTC CTGTTGATGC 120
 CTGGCCCCTG TGGTGGGCTG TTTCACTCCC TATACAGAAG TGTTTCCATG CCACCTAAGG 180
 GAGACTCAGG ACAGCCATTA TTTCTCACCC CTTACATTGA AGCTGGGAAG ATTTATACAG 240
 GCACTAATTC AGTTTTCAG ATATTTCCCTG AATATAAAAA TAATGACTTT TATGTCACTG 300
 GGGAGTCTTA TGCAGGGAAA TATGTGCCAG CCAATGCACA CCTCATCCAT TCCCTCAACC 360
 CTGTGAGAGA GGTGAAGATC AACCTGAACG GAATTGCTAT TGGAGATGGA TATTCTGATC 420
 CCGAATCAAT TATAGGGGCG TATGCAGAAT TCCTGTACCA AATTGGCTTG TTGGATGAGA 480
 AGCAAAAAAA GTACTTCCAG AAGCAGTGCC ATGAATGCAT AGAACACATC AGGAAGCAGA 540
 ACTGGTTTGA GGCCTTTGAA ATACTGGATA AACTACTAGA TGGCGACTTA ACAAGTGATC 600
 CTTCTTACTT CCAGAATGTT ACAGGATGTA GTAATTACTA TAACTTTTTG CGGTGCACGG 660
 AACCTGAGGA TCAGCTTTAC TATGTGAAAT TTTTGTCACT CCCAGAGGTG AGACAAGCCA 720
 TCCACGTGGG GAATCAGACT TTTAATGATG GAACTATAGT TGAAAAGTAC TTGCGAGAAG 780
 ATACAGTACA GTCAGTTAAG CCATGGTTAA CTGAAATCAT GAATAATTAT AAGGTTCTGA 840
 TCTACAATGG CCAACTGGAC ATCATCGTGG CAGCTGCCCT GACAGAGCGC TCCTTGATGG 900
 GCATGGACTG GAAAGGATCC CAGGAATACA AGAAGGCAGA AAAAAAGTT TGGAAAGATCT 960
 TTAAATCTGA CAGTGAAGTG GCTGGTTACA TCCGGCAAGT GGGTGACTTC CATCAGGTAA 1020
 TTATTCGAGG TGGAGGACAT ATTTTACCCCT ATGACCAGCC TCTGAGAGCT TTGACATGA 1080
 TTAATCGATT CATTATGGA AAAGGATGGG ATCCTTATGT TGGATAAACT ACCTTCCCAA 1140
 AAGAGAACAT CAGAGGTTTT CATTGCTGAA AAGAAAATCG TAAAAACAGA AAATGTCATA 1200
 GGAATAAAAA AATTATCTTT TCATATCTGC AAGATTTTTT TCATCAATAA AAATTATCCT 1260
 TGA 1263

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1718107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Val Lys Phe His Leu Leu Val Leu Ile Ala Phe Thr Cys Tyr Thr
 1 5 10 15
 Cys Ser Asp Ala Thr Leu Trp Asn Pro Tyr Lys Lys Leu Met Arg Gly
 20 25 30
 Ser Ala Ser Pro Pro Arg Pro Gly Glu Ser Gly Glu Pro Leu Phe Leu
 35 40 45
 Thr Pro Leu Leu Gln Asp Gly Lys Ile Glu Glu Ala Arg Asn Lys Ala
 50 55 60
 Arg Val Asn His Pro Met Leu Ser Ser Val Glu Ser Tyr Ser Gly Phe
 65 70 75 80
 Met Thr Val Asp Ala Lys His Asn Ser Asn Leu Phe Phe Trp Tyr Val
 85 90 95
 Pro Ala Lys Asn Asn Arg Glu Gln Ala Pro Ile Leu Val Trp Leu Gln
 100 105 110
 Gly Gly Pro Gly Ala Ser Ser Leu Phe Gly Met Phe Glu Glu Asn Gly
 115 120 125
 Pro Phe His Ile His Arg Asn Lys Ser Val Lys Gln Arg Glu Tyr Ser
 130 135 140
 Trp His Gln Asn His His Met Ile Tyr Ile Asp Asn Pro Val Gly Thr
 145 150 155 160
 Gly Phe Ser Phe Thr Asp Ser Asp Glu Gly Tyr Ser Thr Asn Glu Glu
 165 170 175

His Val Gly Glu Asn Leu Met Lys Phe Ile Gln Gln Phe Phe Val Leu
 180 185 190
 Phe Pro Asn Leu Leu Lys His Pro Phe Tyr Ile Ser Gly Glu Ser Tyr
 195 200 205
 Gly Gly Lys Phe Val Pro Ala Phe Gly Tyr Ala Ile His Asn Ser Gln
 210 215 220
 Ser Gln Pro Lys Ile Asn Leu Gln Gly Leu Ala Ile Gly Asp Gly Tyr
 225 230 235 240
 Thr Asp Pro Leu Asn Gln Leu Asn Tyr Gly Glu Tyr Leu Tyr Glu Leu
 245 250 255
 Gly Leu Ile Asp Leu Asn Gly Arg Lys Lys Phe Asp Glu Asp Thr Ala
 260 265 270
 Ala Ala Ile Ala Cys Ala Glu Arg Lys Asp Met Asn Ser Ala Asn Arg
 275 280 285
 Leu Ile Gln Gly Leu Phe Asp Gly Leu Asp Gly Gln Glu Ser Tyr Phe
 290 295 300
 Lys Lys Val Thr Gly Phe Ser Ser Tyr Tyr Asn Phe Ile Lys Gly Asp
 305 310 315 320
 Glu Glu Ser Lys Gln Asp Ser Val Leu Met Glu Phe Leu Ser Asn Pro
 325 330 335
 Glu Val Arg Lys Gly Ile His Val Gly Glu Leu Pro Phe His Asp Ser
 340 345 350
 Asp Gly His Asn Lys Val Ala Glu Met Leu Ser Glu Asp Thr Leu Asp
 355 360 365
 Thr Val Ala Pro Trp Val Ser Lys Leu Leu Ser His Tyr Arg Val Leu
 370 375 380
 Phe Tyr Asn Gly Gln Leu Asp Ile Ile Cys Ala Tyr Pro Met Thr Val
 385 390 395 400
 Asp Phe Leu Met Lys Met Pro Phe Asp Gly Asp Ser Glu Tyr Lys Arg
 405 410 415
 Ala Asn Arg Glu Ile Tyr Arg Val Asp Gly Glu Ile Ala Gly Tyr Lys
 420 425 430
 Lys Arg Ala Gly Arg Leu Gln Glu Val Leu Ile Arg Asn Ala Gly His
 435 440 445
 Met Val Pro Arg Asp Gln Pro Lys Trp Ala Phe Asp Met Ile Thr Ser
 450 455 460
 Phe Thr His Lys Asn Tyr Leu
 465 470

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 190283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro Asp Gln
 20 25 30
 Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser Phe Arg
 35 40 45

Gln	Tyr	Ser	Gly	Tyr	Leu	Lys	Ser	Ser	Gly	Ser	Lys	His	Leu	His	Tyr	50	55	60
Trp	Phe	Val	Glu	Ser	Gln	Lys	Asp	Pro	Glu	Asn	Ser	Pro	Val	Val	Leu	65	70	75
Trp	Leu	Asn	Gly	Gly	Pro	Gly	Cys	Ser	Ser	Leu	Asp	Gly	Leu	Leu	Thr	85	90	95
Glu	His	Gly	Pro	Phe	Leu	Val	Gln	Pro	Asp	Gly	Val	Thr	Leu	Glu	Tyr	100	105	110
Asn	Pro	Tyr	Ser	Trp	Asn	Leu	Ile	Ala	Asn	Val	Leu	Tyr	Leu	Glu	Ser	115	120	125
Pro	Ala	Gly	Val	Gly	Phe	Ser	Tyr	Ser	Asp	Asp	Lys	Phe	Tyr	Ala	Thr	130	135	140
Asn	Asp	Thr	Glu	Val	Ala	Gln	Ser	Asn	Phe	Glu	Ala	Leu	Gln	Asp	Phe	145	150	155
Phe	Arg	Leu	Phe	Pro	Glu	Tyr	Lys	Asn	Asn	Lys	Leu	Phe	Leu	Thr	Gly	165	170	175
Glu	Ser	Tyr	Ala	Gly	Ile	Tyr	Ile	Pro	Thr	Leu	Ala	Val	Leu	Val	Met	180	185	190
Gln	Asp	Pro	Ser	Met	Asn	Leu	Gln	Gly	Leu	Ala	Val	Gly	Asn	Gly	Leu	195	200	205
Ser	Ser	Tyr	Glu	Gln	Asn	Asp	Asn	Ser	Leu	Val	Tyr	Phe	Ala	Tyr	Tyr	210	215	220
His	Gly	Leu	Leu	Gly	Asn	Arg	Leu	Trp	Ser	Ser	Leu	Gln	Thr	His	Cys	225	230	235
Cys	Ser	Gln	Asn	Lys	Cys	Asn	Phe	Tyr	Asp	Asn	Lys	Asp	Leu	Glu	Cys	245	250	255
Val	Thr	Asn	Leu	Gln	Glu	Val	Ala	Arg	Ile	Val	Gly	Asn	Ser	Gly	Leu	260	265	270
Asn	Ile	Tyr	Asn	Leu	Tyr	Ala	Pro	Cys	Ala	Gly	Gly	Val	Pro	Ser	His	275	280	285
Phe	Arg	Tyr	Glu	Lys	Asp	Thr	Val	Val	Val	Gln	Asp	Leu	Gly	Asn	Ile	290	295	300
Phe	Thr	Arg	Leu	Pro	Leu	Lys	Arg	Met	Trp	His	Gln	Ala	Leu	Leu	Arg	305	310	315
Ser	Gly	Asp	Lys	Val	Arg	Met	Asp	Pro	Pro	Cys	Thr	Asn	Thr	Thr	Ala	325	330	335
Ala	Ser	Thr	Tyr	Leu	Asn	Asn	Pro	Tyr	Val	Arg	Lys	Ala	Leu	Asn	Ile	340	345	350
Pro	Glu	Gln	Leu	Pro	Gln	Trp	Asp	Met	Cys	Asn	Phe	Leu	Val	Asn	Leu	355	360	365
Gln	Tyr	Arg	Arg	Leu	Tyr	Arg	Ser	Met	Asn	Ser	Gln	Tyr	Leu	Lys	Leu	370	375	380
Leu	Ser	Ser	Gln	Lys	Tyr	Gln	Ile	Leu	Leu	Tyr	Asn	Gly	Asp	Val	Asp	385	390	395
Met	Ala	Cys	Asn	Phe	Met	Gly	Asp	Glu	Trp	Phe	Val	Asp	Ser	Leu	Asn	405	410	415
Gln	Lys	Met	Glu	Val	Gln	Arg	Arg	Pro	Trp	Leu	Val	Lys	Tyr	Gly	Asp	420	425	430
Ser	Gly	Glu	Gln	Ile	Ala	Gly	Phe	Val	Lys	Glu	Phe	Ser	His	Ile	Ala	435	440	445
Phe	Leu	Thr	Ile	Lys	Gly	Ala	Gly	His	Met	Val	Pro	Thr	Asp	Lys	Pro	450	455	460
Leu	Ala	Ala	Phe	Thr	Met	Phe	Ser	Arg	Phe	Leu	Asn	Lys	Gln	Pro	Tyr	465	470	475
																		480